VERSION WITH MARKINGS TO SHOW CHANGES MADE

Cancel claims 39, 61-68 without prejudice.

34. **(Amended)** A method for determining the identity of **a** ~~the~~ polymorphic nucleotide in a target sequence having at least two known variants, comprising:

obtaining a sample comprising said target sequence;

hybridizing a primer upstream of said polymorphic nucleotide;

performing a first extension reaction with said hybridized primer in the absence of a deoxyribonucleoside triphosphate (dNTP) or ribonucleoside triphosphate (rNTP) complementary to said first known variant, but in the presence of at least one dNTP or rNTP ~~wherein said at least one dNTP or rNTP includes a dNTP or rNTP~~ complementary to said second known variant, ~~and~~ wherein said ~~at least one~~ dNTP or rNTP **complementary to said second known variant** is not detectably labeled or modified**, and wherein the first extension reaction is performed in the absence of a dideoxynucleoside triphosphate (ddNTP)** ;

performing a second extension reaction with said hybridized primer in the absence of a dNTP or rNTP complementary to said second known variant, but in the presence of at least one dNTP or rNTP~~, wherein said at least one dNTP or rNTP includes a dNTP or rNTP~~ complementary to said first known variant, ~~and~~ wherein said ~~at least one~~ dNTP or rNTP **complementary to said first known variant** is not detectably labeled or modified**, and wherein the second extension reaction is performed in the absence of a ddNTP**; and

analyzing the reaction products of said first extension reaction and said second extension reaction.

51. **(Amended)** The method of claim 34, wherein said target sequence having at least two known variants comprises a biallelic marker associated with genetic disorders.

56. **(Amended)** A method for screening a DNA sample for a plurality of target sequences having at least two known variants, comprising:

obtaining a sample comprising a plurality of known target sequences;

hybridizing a primer upstream of each of said target sequences, each primer having a length such that said primer and any extension product thereof can be distinguished from the other primers and any extension products thereof;

performing a plurality of extension reactions wherein each extension reaction contains a single free ~~dNTP or rNTP~~ **deoxyribonucleoside triphosphate (dNTP) or ribonucleoside triphosphate (rNTP)** species complementary to one polymorphic nucleotide of said variant, wherein said single free dNTP or rNTP species is not detectably labeled or modified**, and wherein the plurality of extension reactions are performed in the absence of a dideoxynucleoside triphosphate (ddNTP)**; and

analyzing the reaction products of each extension reaction.

69. **(Amended)** A method for determining the identity of the polymorphic nucleotide in a target sequence having at least two known variants, comprising

performing a primer extension reaction in the absence of a ~~dNTP or rNTP~~ **deoxyribonucleoside triphosphate (dNTP) or ribonucleoside triphosphate (rNTP)** complementary to one of said polymorphic nucleotides but in the presence of at least one dNTP or rNTP complementary to the other polymorphic nucleotide, wherein said at least one dNTP or rNTP complementary to the other polymorphic nucleotide is not detectably labeled or modified, **and wherein the extension reaction is performed in the absence of a dideoxynucleoside triphosphate (ddNTP);** and

detecting the reaction products of said extension reaction.